Amendment to the claims:

Please amend the claims as follows:

1. **(Currently amended)** A method for determining the ~~*Phytophthora sojae* resistance associated with the~~ presence of trait locus Rps8 in a soybean wherein trait locus Rps8 maps to soybean major linkage group F and is associated with soybean resistance to *Phytophthora sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6 and 7, comprising:

analyzing genomic DNA from ~~a~~ the soybean ~~germplasm~~ for the presence of at least ~~one~~ two molecular markers, ~~wherein the at least one molecular marker is~~ associated with ~~the~~ trait locus Rps8, ~~and wherein the trait locus Rps8 maps to soybean major linkage group F and is associated with soybean *Phytophthora sojae* resistance~~ whereby detecting the presence of the molecular markers provides an indication that trait locus Rps8 is present in the soybean.

2. **(Currently amended)** The method of claim 1 wherein the at least ~~one~~ two molecular markers ~~is~~ are selected from the group consisting of Satt516, Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

3. **(Currently amended)** The method of claim 2 wherein the at least ~~one~~ two molecular markers ~~is~~ are markers Satt516 and Satt114.

4. **(Withdrawn)** A method for introgressing soybean *Phytophthora sojae* resistance into non-resistant soybean germplasm or less resistant soybean germplasm comprising:

providing a first soybean germplasm which has Rps8-derived resistance to *Phytophthora sojae* and which has been selected by marker assisted selection using one or more nucleic acid markers, wherein the soybean *Phytophthora sojae* resistance is associated with the Rps8 gene that maps to soybean major linkage group F and wherein the molecular markers are associated with the Rps8 gene;

providing a second soybean germplasm which lacks Rps8-derived resistance to *Phytophthora sojae*;

crossing the first soybean germplasm with the second soybean germplasm to introgress the Rps8 gene into the genome of the second soybean germplasm to provide a hybrid introgressed germplasm having Rps8-derived resistance to *Phytophthora sojae*.

5. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is HFX01-602, or a descendant thereof.

6. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-99128, or a descendant thereof.

7. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-98317, or a descendant thereof.

8. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is selected by a marker assisted selection technique selected from the group consisting of SSR analysis, RFLP analysis, RAPD analyis, and isozyme analysis.

9. **(Withdrawn)** The method of claim 4 wherein the nucleic acid markers are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

10. **(Withdrawn)** A method for the production of a soybean cultivar adapted for conferring, in hybrid combination with a suitable second inbred, resistance to *Phytophthora sojae* comprising:

selecting a first donor parental line possessing the desired *Phytophthora sojae* resistance said first donor parental line comprising a *Phytophthora sojae* resistance gene Rps8 which is located on major linkage group F; crossing the first donor parental line with a second parental

line, which is high yielding in hybrid combination, to produce a segregating plant population of genetically heterogeneous plants;

screening the plants of the segregating plant population for the gene Rps8 by marker assisted selection using at least one associated markers;

selecting plants from the population having the gene Rps8; and

breeding by self crossing the plants containing the Rps8 gene until a line is obtained which is homozygous for resistance to *Phytophthora sojae* at Rps8 to give resistance to *Phytophthora sojae.*

11. **(Withdrawn)** The method of claim 10 wherein the at least one associated marker is selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

12. **(Withdrawn)** The method of claim 10 wherein the molecular markers are Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

13. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is HFX01-602, or a descendant thereof.

14. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-99128, or a descendant thereof.

15. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-98317, or a descendant thereof.

16. **(Withdrawn)** The method of claim 10 wherein the plants of the segregating plant population are screened by a marker assisted selection technique selected the marker assisted selection comprises analyzing by a technique selected from the group consisting of, SSR analysis,.

17. **(Withdrawn)** A method for reliably and predictably introgressing soybean Rps8-derived resistance to *Phytophthora sojae* into susceptible soybean germplasm comprising analyzing soybean germplasm lines by marker assisted selection to identify those soybean germplasm lines having the Rps8 gene; and introgressing said Rps8 gene into said non-resistant soybean germplasm.

18. **(Withdrawn)** The method of claim 18 wherein markers for use in marker assisted selection are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

19. **(Withdrawn)** The method of claim 18 wherein the marker assisted selection comprises the use of SSR analysis.

20. **(Withdrawn)** A soybean plant produced according to the method of any one of claims 1-22.

21. **(Withdrawn)** A soybean plant having resistance to *Phytophthora sojae* comprising:

a soybean germplasm comprising an Rps8 gene

wherein the germplasm was produced by introgression of a soybean germplasm containing Rps8 in its genome with a soybean germplasm lacking the Rps8 gene in its genome.

22. **(Cancelled)**

23. **(Withdrawn)** Seed of soybean germplasm designated OX-98317, deposited as ATCC accession number _____, and progeny therefrom..

24. **(Withdrawn)** Seed of soybean germplasm designated OX-99218, deposited as ATCC accession number _____, and progeny therefrom.

25. **(New)** The method of claim 1, wherein the soybean is a progeny resulting from a cross between a first soybean parent having Rps8-associated *Phytophthora sojae* resistance and a second soybean parent that does not have Rps8-associated *Phytophthora sojae* resistance.

26. **(New)** The method of claim 1, wherein trait locus Rps8 is derived from the plant line PI 399073 or a descendant thereof.

27. **(New)** A method of selecting a soybean plant having trait locus Rps8, wherein the soybean plant is a progeny from a cross between a first parent that has Rps8-associated *Phytophthora sojae* resistance and a second parent that does not have Rps8-associated *Phytophthora sojae* resistance, the method comprising the steps of:

(a) detecting a first nucleic acid from the first parent which is genetically linked to trait locus Rps8 wherein trait locus Rps8 is mapped to major linkage group F and is located between molecular markers Satt114 and Satt516; and

(b) selecting the soybean plant progeny comprising the first nucleic acid thereby selecting the soybean plant having trait locus Rps8.

28. **(New)** The method of claim 27, wherein trait locus Rps8 is associated with a marker selected from the group consisting of Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, and Satt144.

29. **(New)** The method of claim 27, wherein detecting the first nucleic acid comprises RFLP, RAPD, AFLP, or microsatellite analysis.

30. **(New)** The method of claim 27, wherein detecting the first nucleic acid comprises hybridization of a second nucleic acid to the first nucleic acid.

31. **(New)** The method of claim 27, wherein trait locus Rps8 is derived from the plant line PI 399073 or a descendant thereof.

32. **(New)** The method of claim 27, wherein trait locus Rps8 is derived from the plant line HFX01-602 or a descendant thereof.

33. **(New)** A method of identifying soybean plants that are likely to have trait locus Rps8, the method comprising detecting a first locus on the genome of the plant which is genetically linked to trait locus Rps8, wherein the first locus maps to major linkage group F and is located between molecular marker Satt114 and Satt516, whereby detecting the first locus in the plant provides an indication that the trait locus Rps8 resistance is present in the plant.

34. **(New)** The method of claim 33, wherein first locus is associated with a marker selected from the group consisting of Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, and Satt144.

35. **(New)** A method of selecting a soybean plant having Rps8-associated *Phytophthora sojae* resistance, wherein the soybean plant is a progeny from a cross between a first parent that has Rps8-associated *Phytophthora sojae* resistance and a second parent that does not have Rps8-associated *Phytophthora sojae* resistance, the method comprising the steps of:

(a) detecting a *Phytophthora sojae* isolate that the second parent is susceptible to, wherein said *Phytophthora sojae* isolate is selected from the group consisting of pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and combinations thereof; and

(b) selecting the progeny that is resistant to said *Phytophthora sojae* isolate, thereby selecting a soybean plant having Rps8- associated *Phytophthora sojae* resistance.

36. **(New)** The method of claim 35, wherein the *Phytophthora sojae* isolate is selected from the group consisting of OH race 1, OH race 4, OH race 17, OH race 25, OH race 30, and combinations thereof.